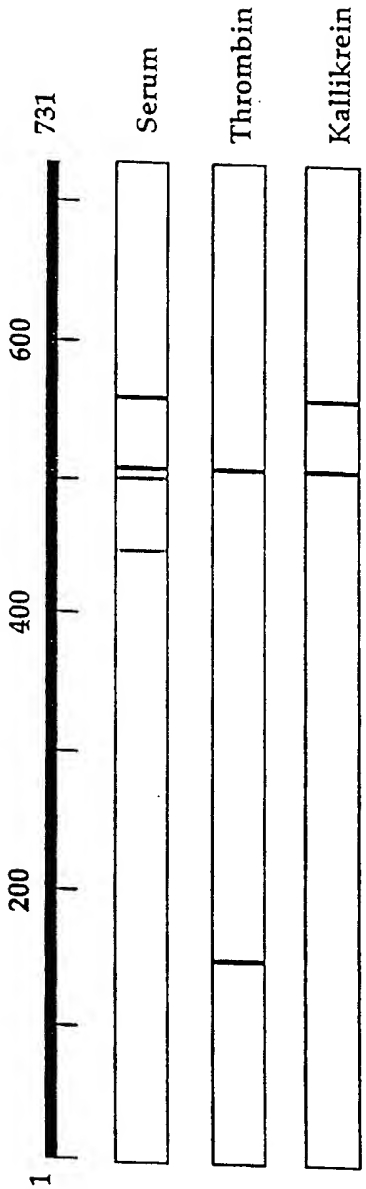


Figure 1

```
1   GATCCATGGGTGGCGTTCCGGGTGCTATCCCGGGTGGCGTTCCGGGTGGTGTATTCTACC   60
    GTACCCACCGCAAGGCCCACGATAGGGCCCACCGCAAGGCCCACCACATAAGATGG

    S  M  G  G  V  P  G  A  I  P  G  G  V  P  G  G  V  F  Y  P
          ↑ Start pf mature processed protein

61  CAGGCGCGGGTCTGGGTGCACTGGGCGGTGGTGCGCTGGGCCCGGGTGGTAAACCGCTGA  120
    GTCCGCGCCCAGACCCACGTGACCCGCCACCACGCGACCCGGGCCCACCATTTGGCGACT

    G  A  G  L  G  A  L  G  G  G  A  L  G  P  G  G  K  P  L  K

121 AACCGGTTCCAGGCGGTCTGGCAGGTGCTGGTCTGGGTGCAGGTCTGGGCGCGTTCCCGG  180
    TTGGCCAAGGTCCGCCAGACCGTCCACGACCAGACCCACGTCCAGACCCGCGCAAGGGCC

    P  V  P  G  G  L  A  G  A  G  L  G  A  G  L  G  A  F  P  A

181 CGGTTACCTTCCCGGGTGCTCTGGTTCCGGGTGGCGTTGCAGACGCAGCTGCTGCGTACA  240
    GCCAATGGAAGGGCCCACGAGACCAAGGCCCACCGCAACGTCTGCGTCGACGACGCATGT

    V  T  F  P  G  A  L  V  P  G  G  V  A  D  A  A  A  A  Y  K

241 AAGCGGCAAAGGCAGGTGCGGGTCTGGGCGGGGTACCAGGTGTTGGCGGTCTGGGTGTAT  300
    TTCGCCGTTTCCGTCCACGCCCAGACCCGCCCCATGGTCCACAACCGCCAGACCCACATA

    A  A  K  A  G  A  G  L  G  G  V  P  G  V  G  G  L  G  V  S

301 CTGCTGGCGCAGTTGTTCCGCAGCCGGGTGCAGGTGTAAAACCGGGCAAAGTTCCAGGTG  360
    GACGACCGCGTCAACAAGGCGTCGGCCCACGTCCACATTTTGGCCCGTTTCAAGGTCCAC

    A  G  A  V  V  P  Q  P  G  A  G  V  K  P  G  K  V  P  G  V

361 TTGGTCTGCCGGGCGTATACCCGGGTGGTGTTCTGCCGGGCGCGCGTTTCCCAGGTGTTG  420
    AACCAGACGGCCCGCATATGGGCCCACCACAAGACGGCCCGCGCGCAAAGGGTCCACAAC

    G  L  P  G  V  Y  P  G  G  V  L  P  G  A  R  F  P  G  V  G
```

Figure 2(a)

```
421  GTGTACTGCCGGGCGTTCCGACCGGTGCAGGTGTTAAACCGAAGGCACCAGGTGTAGGCG   480
     CACATGACGGCCCGCAAGGCTGGCCACGTCCACAATTTGGCTTCCGTGGTCCACATCCGC

       V  L  P  G  V  P  T  G  A  G  V  K  P  K  A  P  G  V  G  G

481  GCGCGTTCGCGGGTATCCCGGGTGTTGGCCCGTTCGGTGGTCCGCAGCCAGGCGTTCCGC   540
     CGCGCAAGCGCCCATAGGGCCCACAACCGGGCAAGCCACCAGGCGTCGGTCCGCAAGGCG

       A  F  A  G  I  P  G  V  G  P  F  G  G  P  Q  P  G  V  P  L

541  TGGGTTACCCGATCAAAGCGCCGAAGCTTCCAGGTGGCTACGGTCTGCCGTACACCACCG   600
     ACCCAATGGGCTAGTTTCGCGGCTTCGAAGGTCCACCGATGCCAGACGGCATGTGGTGGC

       G  Y  P  I  K  A  P  K  L  P  G  G  Y  G  L  P  Y  T  T  G

601  GTAAACTGCCGTACGGCTACGGTCCGGGTGGCGTAGCAGGTGCTGCGGGTAAAGCAGGCT   660
     CATTTGACGGCATGCCGATGCCAGGCCCACCGCATCGTCCACGACGCCCATTTCGTCCGA

       K  L  P  Y  G  Y  G  P  G  G  V  A  G  A  A  G  K  A  G  Y

661  ACCCAACCGGTACTGGTGTTGGTCCGCAGGCTGCTGCGGCAGCTGCGGCGAAGGCAGCAG   720
     TGGGTTGGCCATGACCACAACCAGGCGTCCGACGACGCCGTCGACGCCGCTTCCGTCGTC

       P  T  G  T  G  V  G  P  Q  A  A  A  A  A  A  A  K  A  A  A

721  CAAAATTCGGCGCGGGTGCAGCGGGTGTTCTGCCGGGCGTAGGTGGTGCTGGCGTTCCGG   780
     GTTTTAAGCCGCGCCCACGTCGCCCACAAGACGGCCCGCATCCACCACGACCGCAAGGCC

       K  F  G  A  G  A  A  G  V  L  P  G  V  G  G  A  G  V  P  G

781  GTGTTCCAGGTGCGATCCCGGGCATCGGTGGTATCGCAGGCGTAGGTACTCCGGCGGCCG   840
     CACAAGGTCCACGCTAGGGCCCGTAGCCACCATAGCGTCCGCATCCATGAGGCCGCCGGC

       V  P  G  A  I  P  G  I  G  G  I  A  G  V  G  T  P  A  A  A

841  CTGCGGCTGCGGCAGCTGCGGCGAAAGCAGCTAAATACGGTGCGGCAGCAGGCCTGGTTC   900
     GACGCCGACGCCGTCGACGCCGCTTTCGTCGATTTATGCCACGCCGTCGTCCGGACCAAG

       A  A  A  A  A  A  A  K  A  A  K  Y  G  A  A  A  G  L  V  P
```

Figure 2(b)

```
901  CGGGTGGTCCAGGCTTCGGTCCGGGTGTTGTAGGCGTTCCGGGTGCTGGTGTTCCGGGCG  960
     GCCCACCAGGTCCGAAGCCAGGCCCACAACATCCGCAAGGCGCACGACCACAAGGCCCGC

       G  G  P  G  F  G  P  G  V  V  G  V  P  G  A  G  V  P  G  V

961  TAGGTGTTCCAGGTGCGGGCATCCCGGTTGTACCGGGTGCAGGTATCCCGGGCGCTGCGG  1020
     ATCCACAAGGTCCACGCCCGTAGGGCCAACATGGCCCACGTCCATAGGGCCCGCGACGCC

       G  V  P  G  A  G  I  P  V  V  P  G  A  G  I  P  G  A  A  V

1021 TTCCAGGTGTTGTATCCCCGGAAGCGGCAGCTAAGGCTGCTGCGAAAGCTGCGAAATACG  1080
     AAGGTCCACAACATAGGGGCCTTCGCCGTCGATTCCGACGACGCTTTCGACGCTTTATGC

       P  G  V  V  S  P  E  A  A  A  K  A  A  A  K  A  A  K  Y  G

1081 GAGCTCGTCCGGGCGTTGGTGTTGGTGGCATCCCGACCTACGGTGTAGGTGCAGGCGGTT  1140
     CTCGAGCAGGCCCGCAACCACAACCACCGTAGGGCTGGATGCCACATCCACGTCCGCCAA

       A  R  P  G  V  G  V  G  G  I  P  T  Y  G  V  G  A  G  G  F

1141 TCCCAGGTTTCGGCGTTGGTGTTGGTGGCATCCCGGGTGTAGCTGGTGTTCCGTCTGTTG  1200
     AGGGTCCAAAGCCGCAACCACAACCACCGTAGGGCCCACATCGACCACAAGGCAGACAAC

       P  G  F  G  V  G  V  G  G  I  P  G  V  A  G  V  P  S  V  G

1201 GTGGCGTACCGGGTGTTGGTGGCGTTCCAGGTGTAGGTATCTCCCCGGAAGCGCAGGCAG  1260
     CACCGCATGGCCCACAACCACCGCAAGGTCCACATCCATAGAGGGGCCTTCGCGTCCGTC

       G  V  P  G  V  G  G  V  P  G  V  G  I  S  P  E  A  Q  A  A

1261 CTGCGGCAGCTAAAGCAGCGAAGTACGGCGTTGGTACTCCGGCGGCAGCAGCTGCTAAAG  1320
     GACGCCGTCGATTTCGTCGCTTCATGCCGCAACCATGAGGCCGCCGTCGTCGACGATTTC

       A  A  A  K  A  A  K  Y  G  V  G  T  P  A  A  A  A  A  K  A

1321 CAGCGGCTAAAGCAGCGCAGTTCGGACTAGTTCCGGGCGTAGGTGTTGCGCCAGGTGTTG  1380
     GTCGCCGATTTCGTCGCGTCAAGCCTGATCAAGGCCCGCATCCACAACGCGGTCCACAAC

       A  A  K  A  A  Q  F  G  L  V  P  G  V  G  V  A  P  G  V  G
```

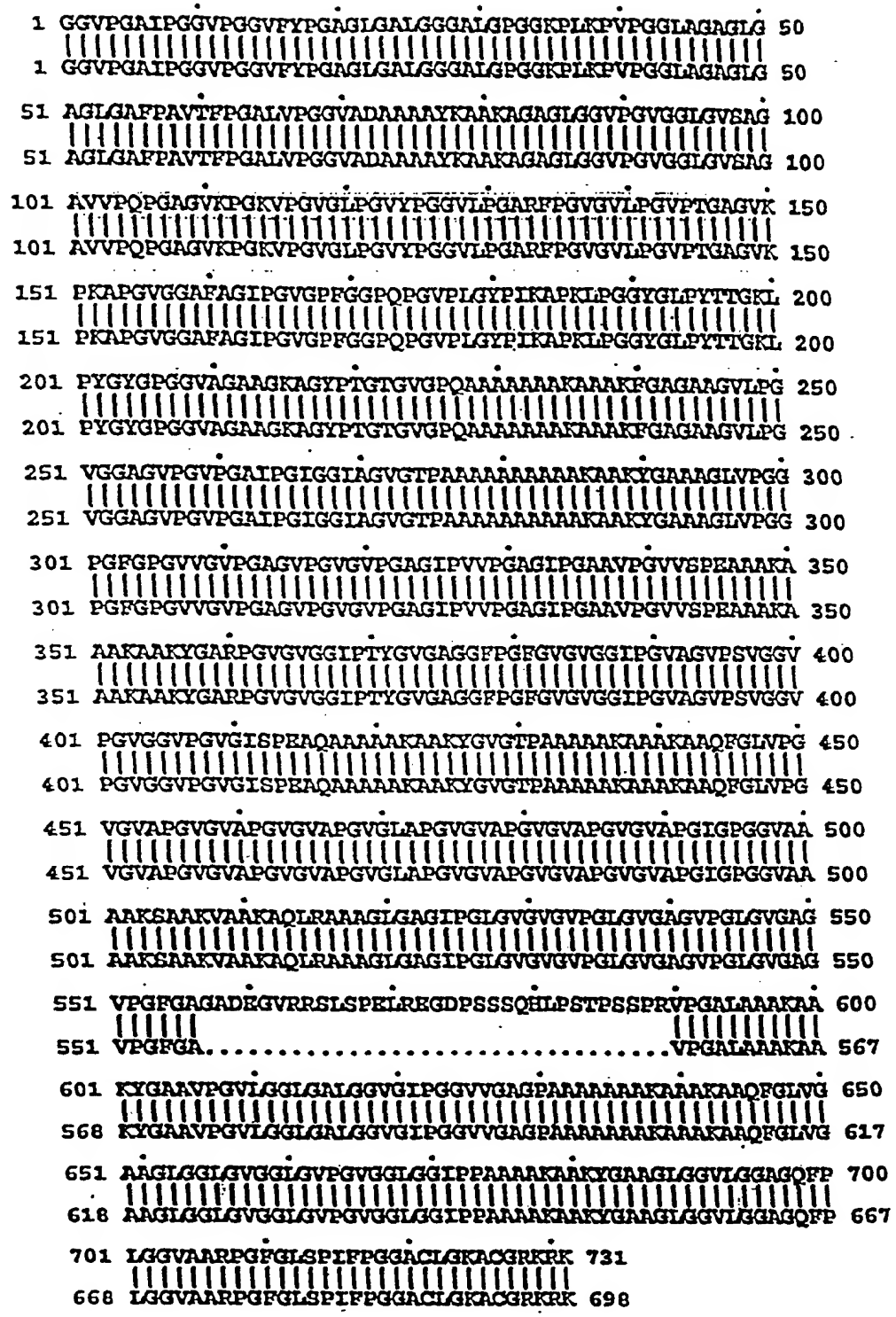
Figure 2(c)

```
1381  GCGTAGCACCGGGTGTTGGTGTTGCTCCGGGCGTAGGTCTGGCACCGGGTGTTGGCGTTG  1440
      CGCATCGTGGCCCACAACCACAACGAGGCCCGCATCCAGACCGTGGCCCACAACCGCAAC

        V  A  P  G  V  G  V  A  P  G  V  G  L  A  P  G  V  G  V  A

1441  CACCAGGTGTAGGTGTTGCGCCGGGCGTTGGTGTAGCACCGGGTATCGGTCCGGGTGGCG  1500
      GTGGTCCACATCCACAACGCGGCCCGCAACCACATCGTGGCCCATAGCCAGGCCCACCGC

        P  G  V  G  V  A  P  G  V  G  V  A  P  G  I  G  P  G  G  V

1501  TTGCGGCTGCTGCGAAATCTGCTGCGAAGGTTGCTGCGAAAGCGCAGCTGCGTGCAGCAG  1560
      AACGCCGACGACGCTTTAGACGACGCTTCCAACGACGCTTTCGCGTCGACGCACGTCGTC

        A  A  A  A  K  S  A  A  K  V  A  A  K  A  Q  L  R  A  A  A

1561  CTGGTCTGGGTGCGGGCATCCCAGGTCTGGGTGTAGGTGTTGGTGTTCCGGGCCTGGGTG  1620
      GACCAGACCCACGCCCGTAGGGTCCAGACCCACATCCACAACCACAAGGCCCGGACCCAC

        G  L  G  A  G  I  P  G  L  G  V  G  V  G  V  P  G  L  G  V

1621  TAGGTGCAGGGGTACCGGGCCTGGGTGTTGGTGCAGGCGTTCCGGGTTTCGGTGCTGGCG  1680
      ATCCACGTCCCCATGGCCCGGACCCACAACCACGTCCGCAAGGCCCAAAGCCACGACCGC

        G  A  G  V  P  G  L  G  V  G  A  G  V  P  G  F  G  A  G  A

1681  CGGACGAAGGTGTACGTCGTTCCCTGTCTCCAGAACTGCGTGAAGGTGACCCGTCCTCTT  1740
      GCCTGCTTCCACATGCAGCAAGGGACAGAGGTCTTGACGCACTTCCACTGGGCAGGAGAA

        D  E  G  V  R  R  S  L  S  P  E  L  R  E  G  D  P  S  S  S

1741  CCCAGCACCTGCCGTCTACCCCGTCCTCTCCACGTGTTCCGGGCGCGCTGGCTGCTGCGA  1800
      GGGTCGTGGACGGCAGATGGGGCAGGAGAGGTGCACAAGGCCCGCGCGACCGACGACGCT

        Q  H  L  P  S  T  P  S  S  P  R  V  P  G  A  L  A  A  A  K

1801  AAGCGGCGAAATACGGTGCAGCGGTTCCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCG  1860
      TTCGCCGCTTTATGCCACGTCGCCAAGGCCCACATGACCCGCCAGACCCACGAGACCCGC

        A  A  K  Y  G  A  A  V  P  G  V  L  G  G  L  G  A  L  G  G
```

Figure 2(d)

```
1861  GTGTTGGTATCCCGGGCGGTGTTGTAGGTGCAGGCCCAGCTGCAGCTGCTGCTGCGGCAA  1920
      CACAACCATAGGGCCCGCCACAACATCCACGTCCGGGTCGACGTCGACGACGACGCCGTT
        V  G  I  P  G  G  V  V  G  A  G  P  A  A  A  A  A  A  A  K

1921  AGGCAGCGGCGAAAGCAGCTCAGTTCGGTCTGGTTGGTGCAGCAGGTCTGGGCGGTCTGG  1980
      TCCGTCGCCGCTTTCGTCGAGTCAAGCCAGACCAACCACGTCGTCCAGACCCGCCAGACC
        A  A  A  K  A  A  Q  F  G  L  V  G  A  A  G  L  G  G  L  G

1981  GTGTTGGCGGTCTGGGTGTACCGGGCGTTGGTGGTCTGGGTGGCATCCCGCCGGCGGCGG  2040
      CACAACCGCCAGACCCACATGGCCCGCAACCACCAGACCCACCGTAGGGCGGCCGCCGCC
        V  G  G  L  G  V  P  G  V  G  G  L  G  G  I  P  P  A  A  A

2041  CAGCTAAAGCGGCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGTGCTGGTC  2100
      GTCGATTTCGCCGATTTATGCCACGTCGTCCAGACCCACCGCAAGACCCACCACGACCAG
        A  K  A  A  K  Y  G  A  A  G  L  G  G  V  L  G  G  A  G  Q

2101  AGTTCCCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCTGTCCCCGATCTTCCCAG  2160
      TCAAGGGTGACCCGCCACATCGCCGTGCAGGCCCAAAGCCAGACAGGGGCTAGAAGGGTC
        F  P  L  G  G  V  A  A  R  P  G  F  G  L  S  P  I  F  P  G

2161  GCGGTGCATGCCTGGGTAAAGCTTGCGGCCGTAAACGTAAATAATGATAG            2210
      CGCCACGTACGGACCCATTTCGAACGCCGGCATTTGCATTTATTACTATCCTAG
        G  A  C  L  G  K  A  C  G  R  K  R  K  *  *  *
```

Figure 2(e)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1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLG 50
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51 AGLGAFPAVTFPGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGGLGVSAG 100
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101 AVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK 150
151 PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL 200
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301 PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKA 350
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551 VPGFGA.....VPGALAAAKAA 567
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651 AAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFP 700
618 AAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFP 667
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668 LGGVAARPGFGLSPIFPGGACLGKACGRKRK 698

Figure 3

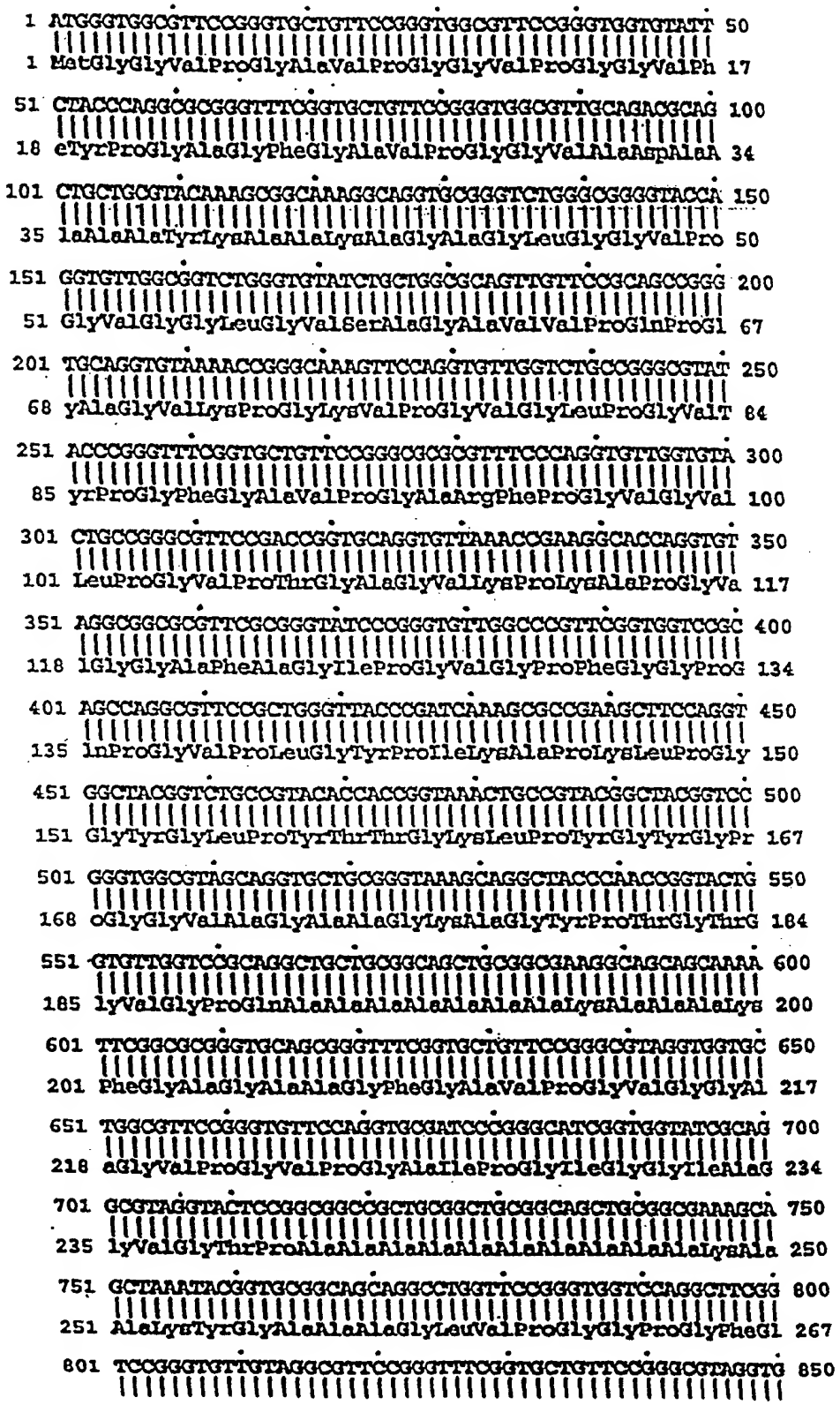
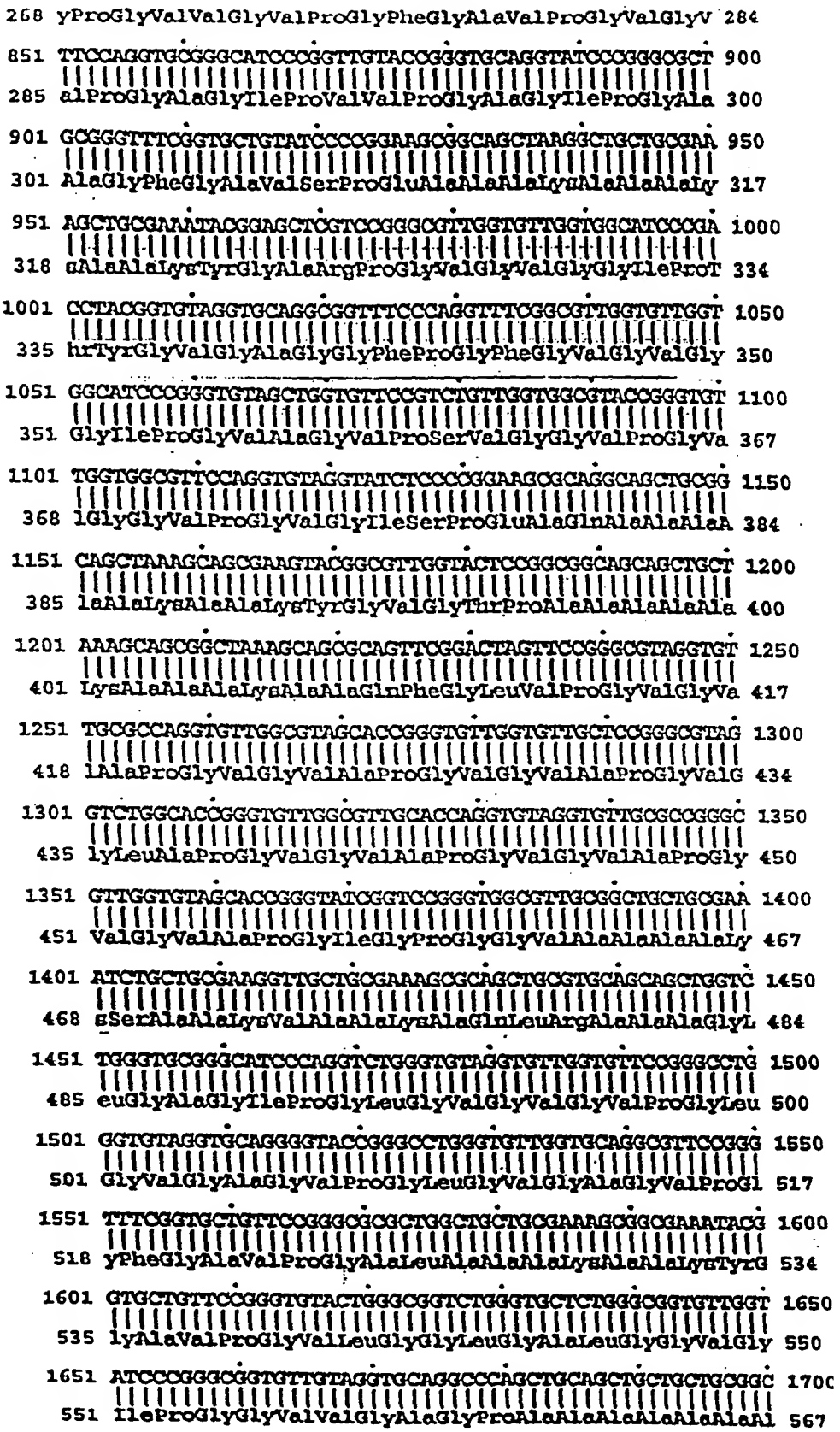


Figure 4(a)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901 GCGGGTTTCGGTGCTGTATCCCCGGAAGCGGCAGCTAAGGCTGCTGCGAA 950
301 AlaGlyPheGlyAlaValSerProGluAlaAlaAlaLysAlaAlaAlaLy 317
951 AGCTGCGAAATACGGAGCTCGTCCGGGCGTTGGTGTTGGTGGCATCCCGA 1000
318 sAlaAlaLysTyrGlyAlaArgProGlyValGlyValGlyGlyIleProT 334
1001 CCTACGGTGTAGGTGCAGGCGGTTTCCCAGGTTTCGGCGTTGGTGTTGGT 1050
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1251 TGCGCCAGGTGTTGGCGTAGCACCGGGTGTTGGTGTTGCTCCGGGCGTAG 1300
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1301 GTCTGGCACCGGGTGTTGGCGTTGCACCAGGTGTAGGTGTTGCGCCGGGC 1350
435 lyLeuAlaProGlyValGlyValAlaProGlyValGlyValAlaProGly 450
1351 GTTGGTGTAGCACCGGGTATCGGTCCGGGTGGCGTTGCGGCTGCTGCGAA 1400
451 ValGlyValAlaProGlyIleGlyProGlyGlyValAlaAlaAlaAlaLy 467
1401 ATCTGCTGCGAAGGTTGCTGCGAAAGCGCAGCTGCGTGCAGCAGCTGGTC 1450
468 sSerAlaAlaLysValAlaAlaLysAlaGlnLeuArgAlaAlaAlaGlyL 484
1451 TGGGTGCGGGCATCCCAGGTCTGGGTGTAGGTGTTGGTGTTCCGGGCCTG 1500
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1551 TTTCGGTGCTGTTCCGGGCGCGCTGGCTGCTGCGAAAGCGGCGAAATACG 1600
518 yPheGlyAlaValProGlyAlaLeuAlaAlaAlaLysAlaAlaLysTyrG 534
1601 GTGCTGTTCCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCGGTGTTGGT 1650
535 lyAlaValProGlyValLeuGlyGlyLeuGlyAlaLeuGlyGlyValGly 550
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Figure 4(b)

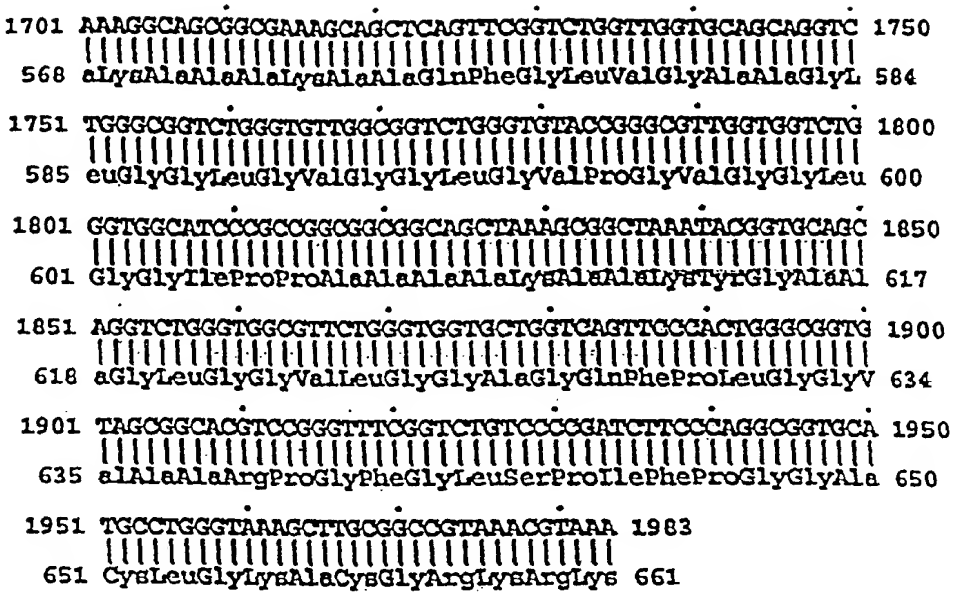
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Figure 4(c)

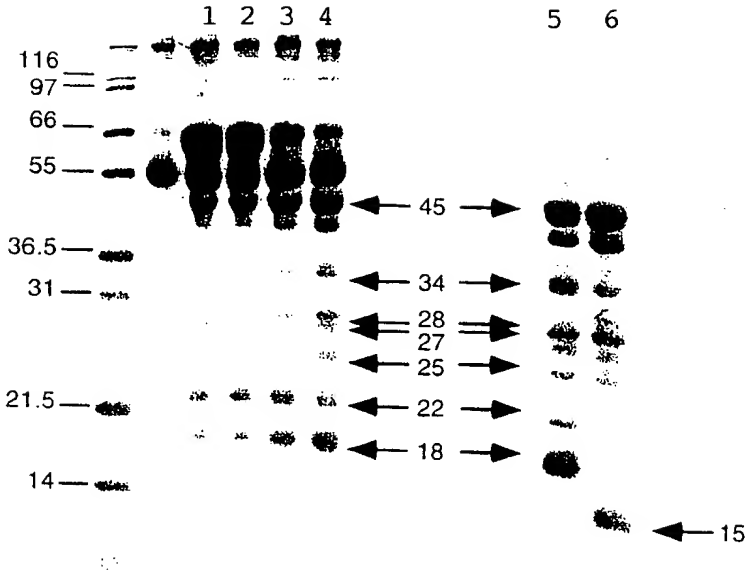
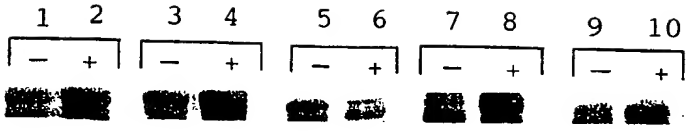


Figure 5



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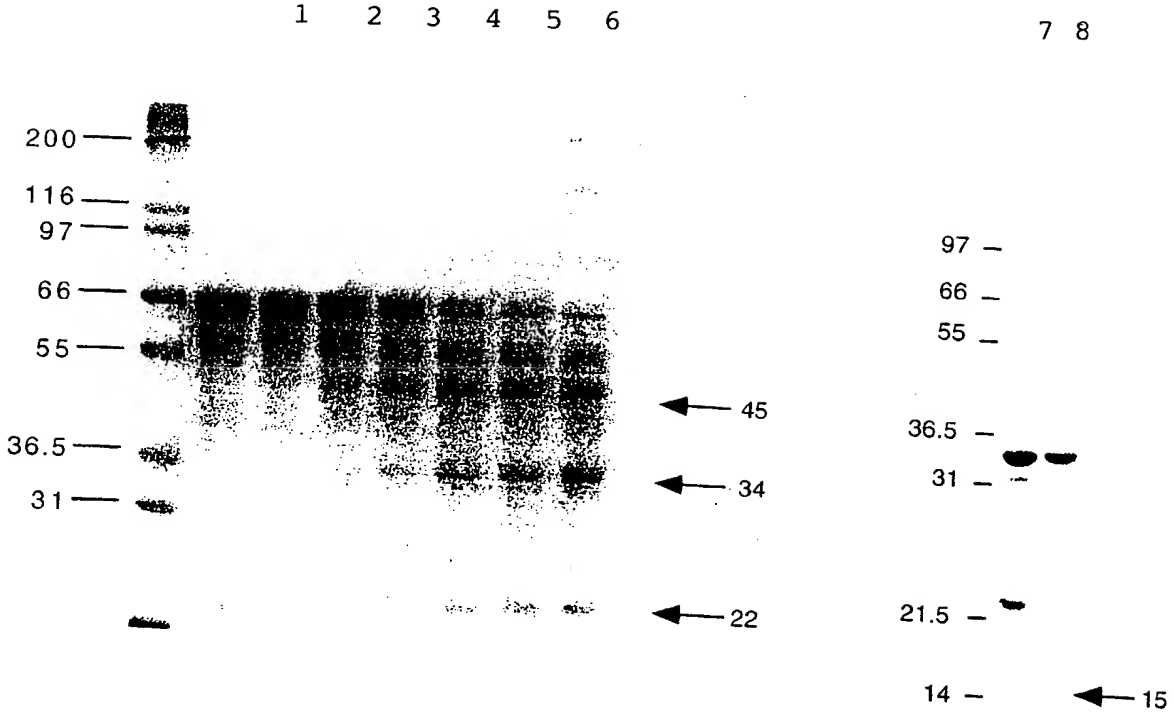

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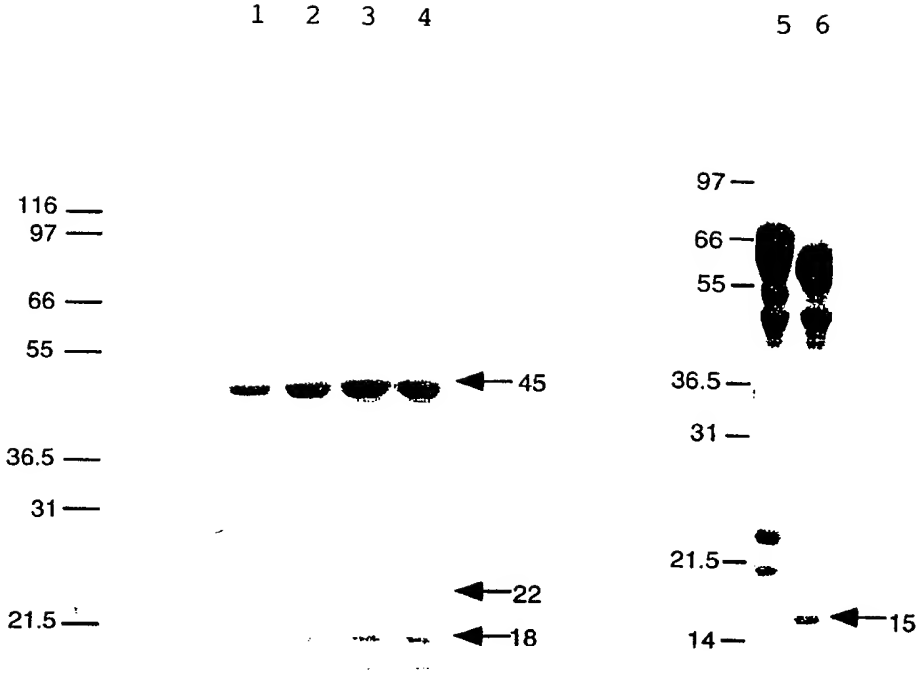

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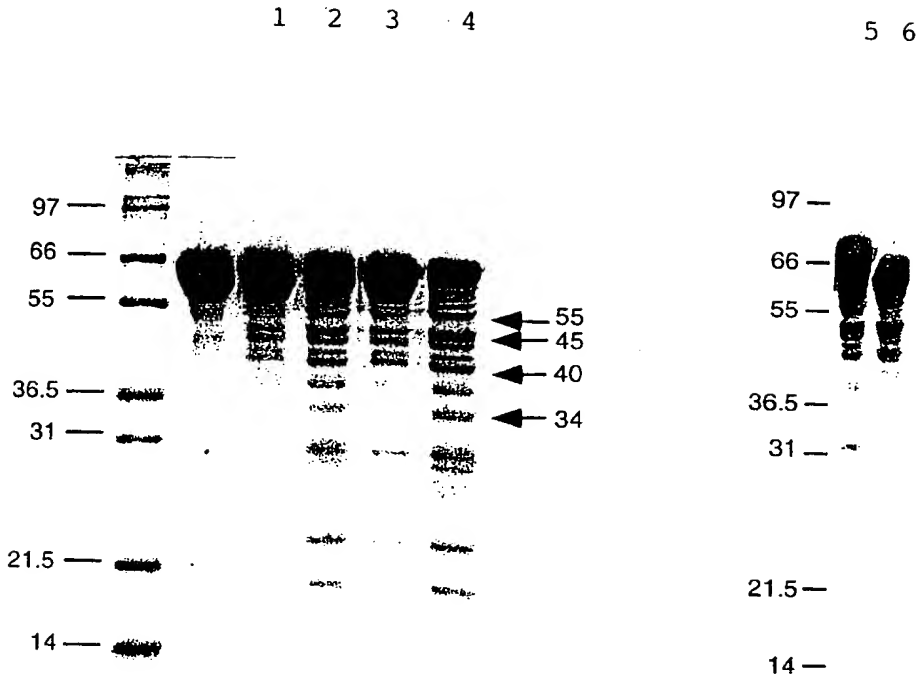

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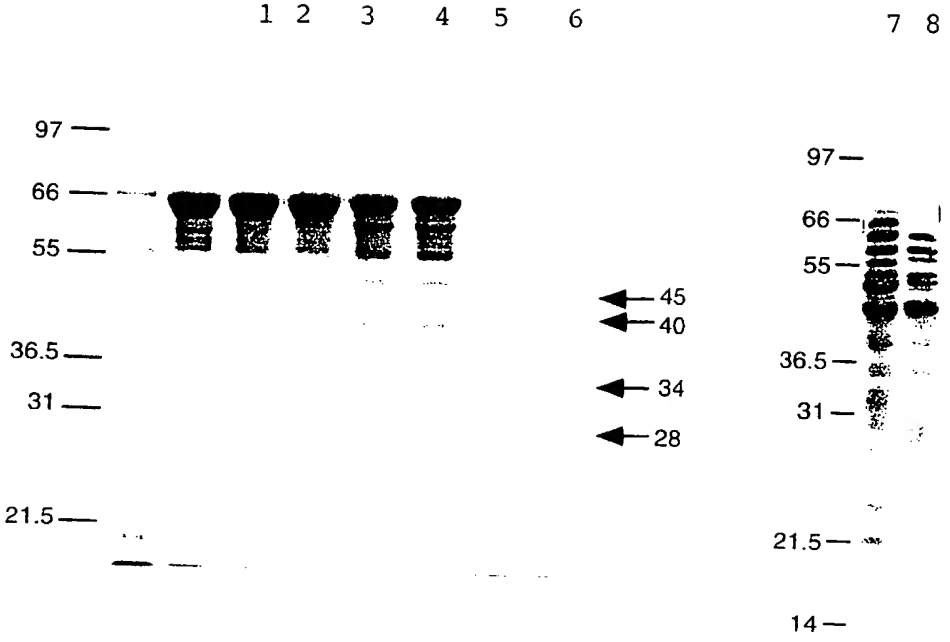

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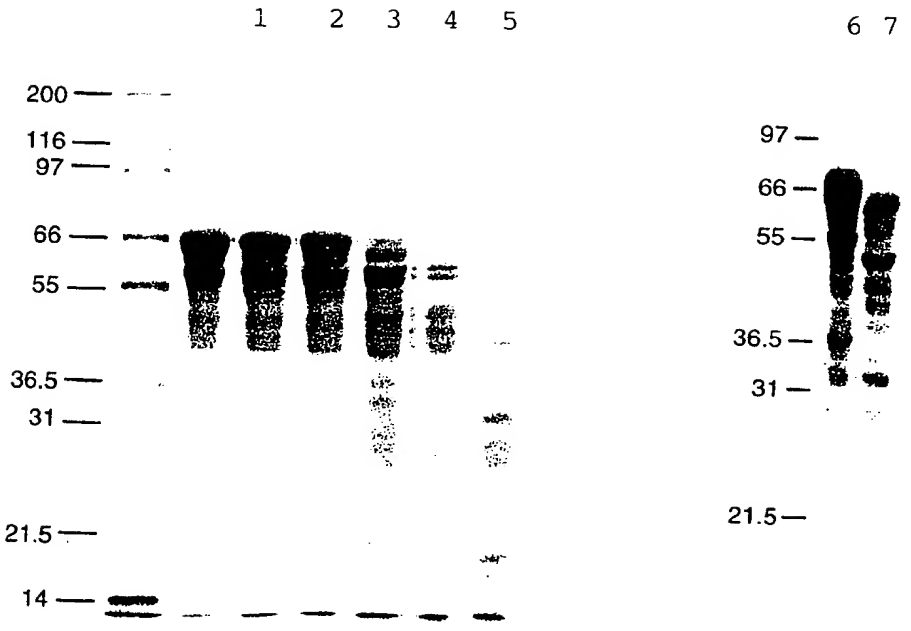
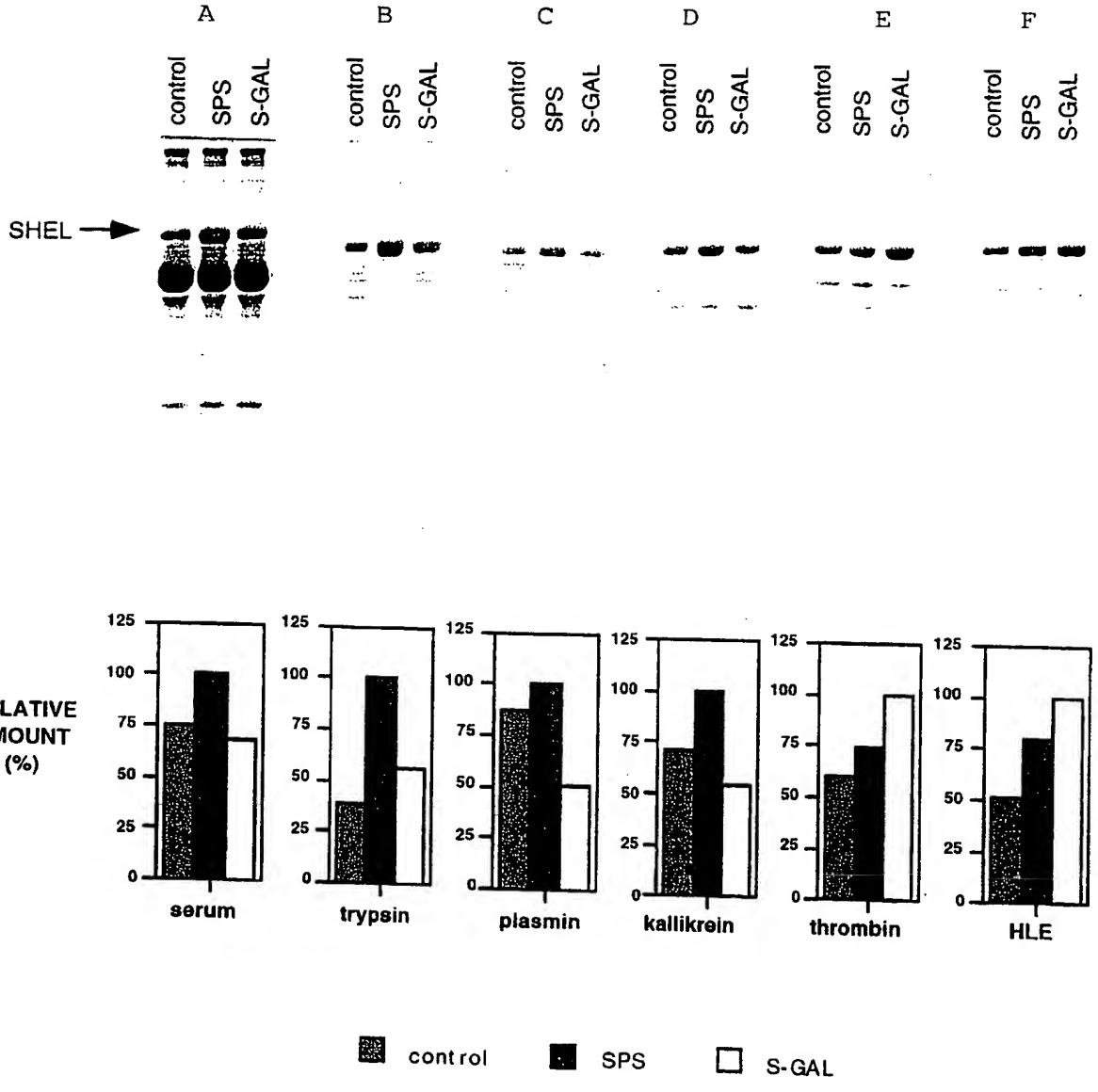


Figure 11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B
C
D
E
F
control
SPS
S-GAL
SHEL
RELATIVE AMOUNT (%)
125
100
75
50
25
0
serum
trypsin
plasmin
kallikrein
thrombin
HLE
control
SPS
S-GAL

Figure 12

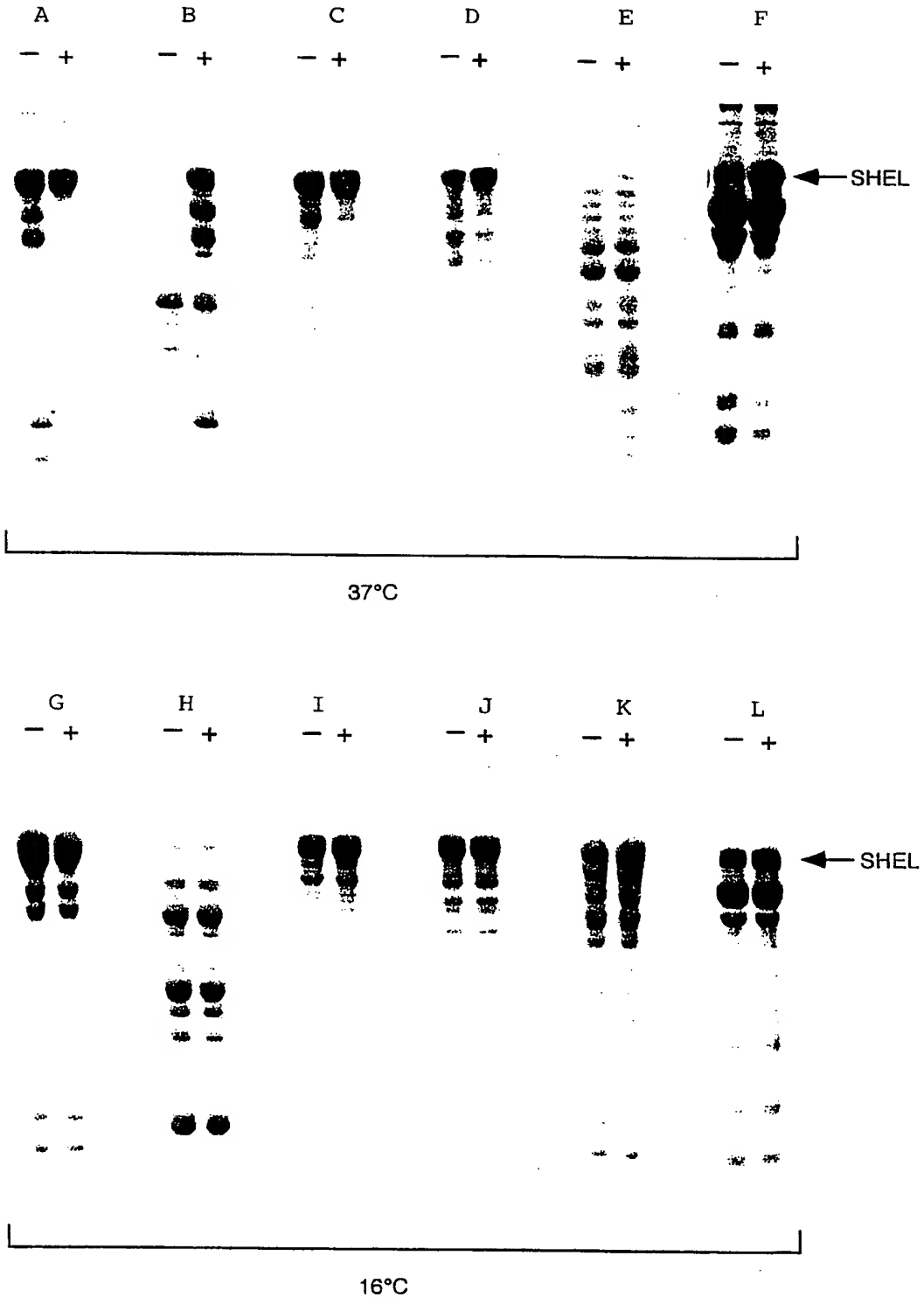

Figure 13

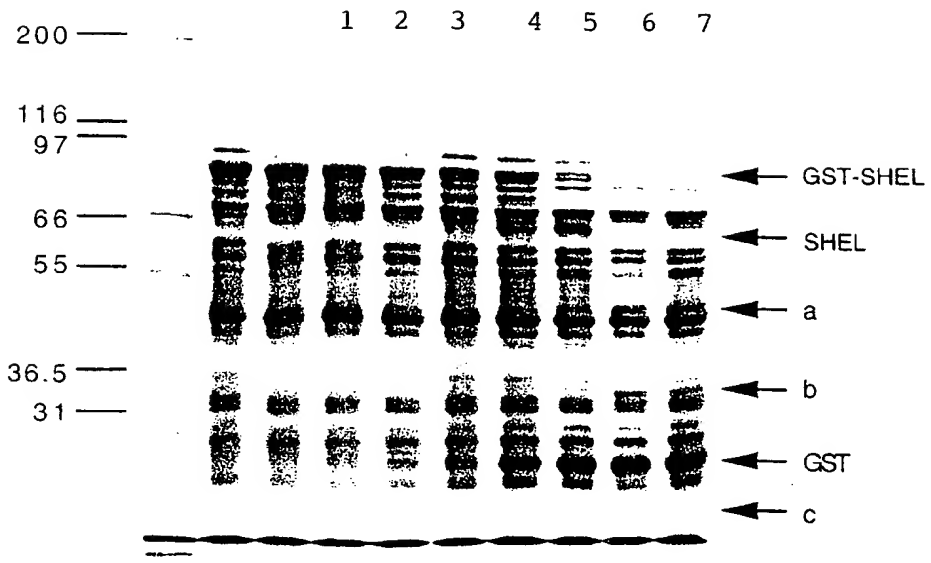

Figure 14

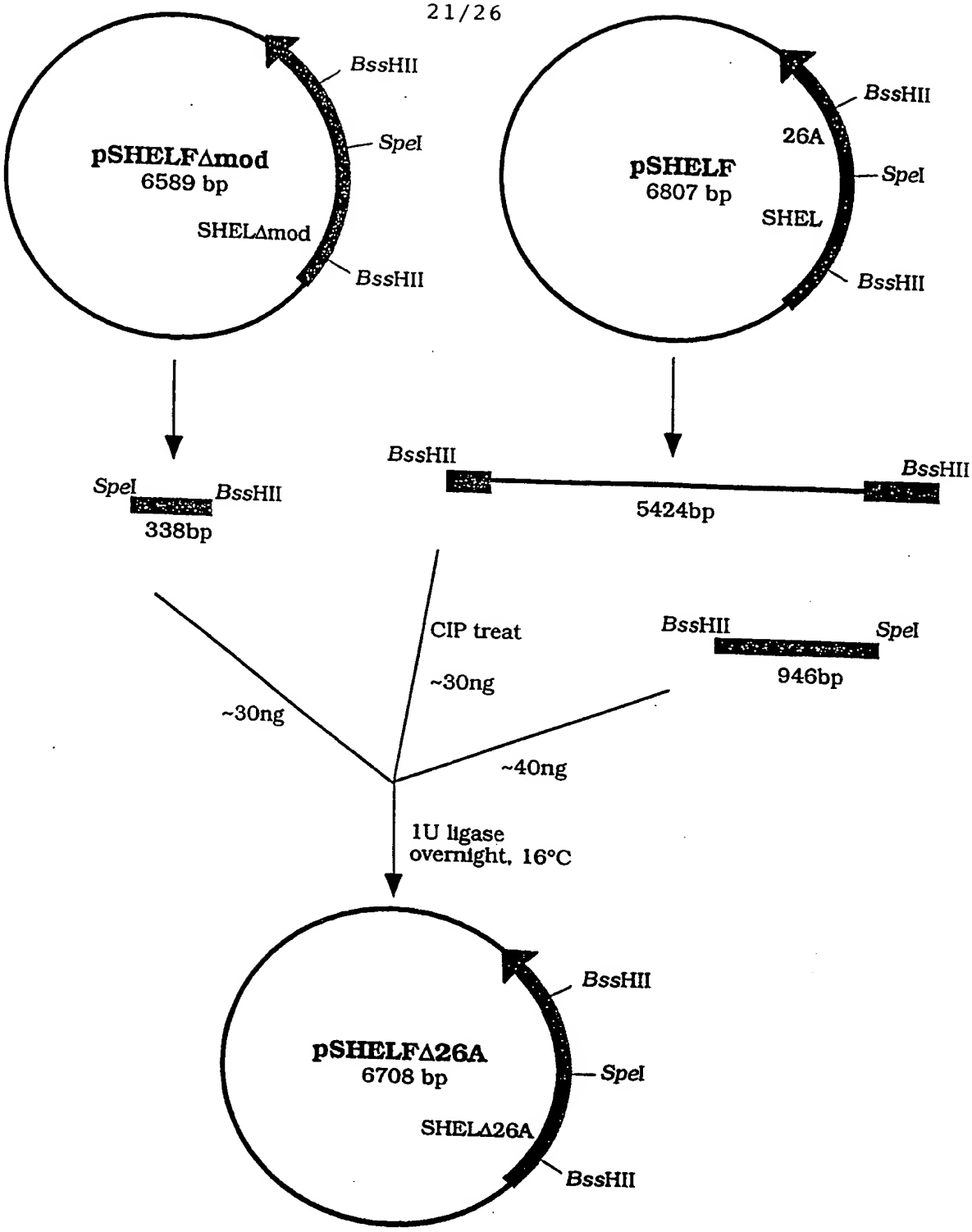
BssHII
SpeI
pSHELFΔmod
6589 bp
SHELΔmod
BssHII
BssHII
26A
SpeI
pSHELF
6807 bp
SHEL
BssHII
SpeI
BssHII
338bp
BssHII
BssHII
5424bp
CIP treat
~30ng
~30ng
~40ng
BssHII
SpeI
946bp
1U ligase
overnight, 16°C
BssHII
pSHELFΔ26A
6708 bp
SpeI
SHELΔ26A
BssHII

Figure 15

Figure 16

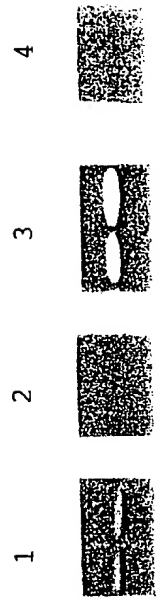

Figure 17

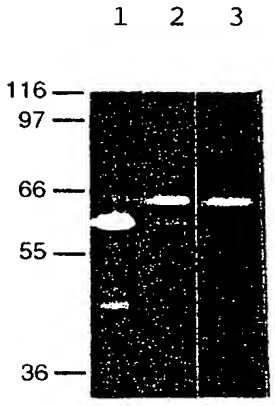

Figure 18

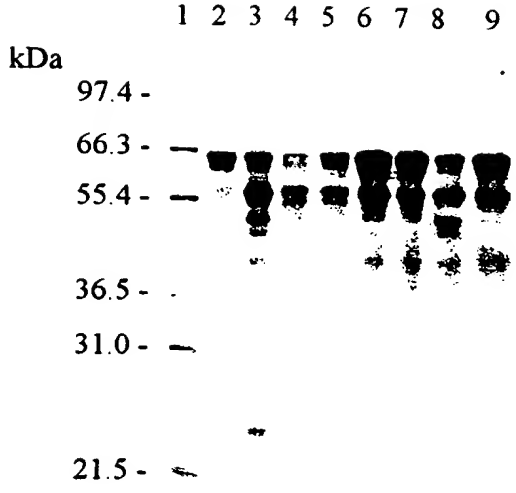

Figure 19

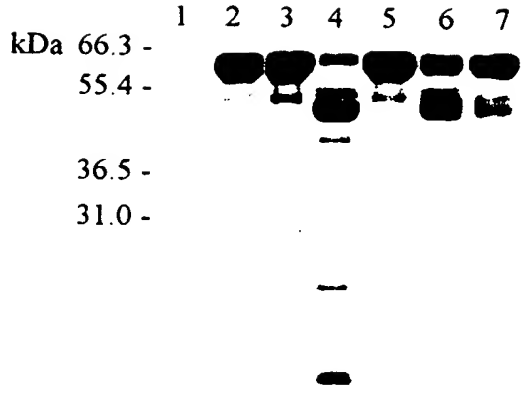

Figure 20